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Minter, Melissa, O'Brien, David, Cottrell, Joan et al. (3 more authors) (Accepted: 2021)
Exploring the potential for 'Gene Conservation Units' to conserve genetic diversity in wild populations. Ecological Solutions and Evidence. ISSN 2688-8319 (In Press)

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Exploring the potential for ‘Gene Conservation Units’ to conserve genetic
diversity in wild populations

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Abstract

1. Genetic diversity is important for species persistence and Gene Conservation Units (GCUs) have been implemented for forest trees to protect genetic diversity and evolutionary processes *in situ*. The Convention on Biological Diversity stipulates the protection of genetic diversity as an Aichi target, and so we explore the potential for GCUs to be implemented more widely.
2. Our global systematic review showed that GCUs are currently implemented primarily for plant species of economic importance (109/158 species studied), but a questionnaire sent to land managers and conservationists (60 UK participants) revealed strong support for fully integrating genetic information into conservation management (90% agree), and for creating GCUs for other plant and animal taxa.
3. Using four case studies of UK species of conservation importance which vary in genetic threat and population dynamics (two insect species, a fungus and a plant), we highlight that GCU implementation criteria need to be flexible to account for variation in effective breeding population size and geographic extent of target species. The wider uptake of GCUs would ensure that threatened genetic diversity is protected and support evolutionary processes that aid adaptation to changing environments.

Keywords

Conservation, genetic diversity, *in situ*, Gene Conservation Unit

1. Introduction

Intra-specific genetic diversity is key in providing populations with the capacity to adapt to changing environmental conditions and to challenges from novel pests and diseases (Barrett & Schluter, 2008; Hoffmann & Sgro, 2011). Genetic diversity may be neutral (no effect on fitness) or adaptive (Holderegger, Kamm, & Gugerli, 2006), and loss of genetic diversity can lead to lower fitness (Reed & Frankham, 2003), changes to physiology (Roelke, Martenson, & O'Brien, 1993), and higher loads of pathogens and infectious diseases (Cunningham et al., 2008). Therefore, conserving genetic diversity is important for mitigating biodiversity loss (Reed & Frankham, 2003) and enabling species to respond to changing environments (Wernberg et al., 2018). Despite its importance, conservation of genetic diversity, and hence local adaptation, is rarely included in policy and conservation management (Laikre, 2010). However, under the Convention of Biological Diversity (CBD), maintenance of genetic variation is an Aichi target (target 13) (CBD, 2011). A recent analysis showed that although many CBD country reports mentioned maintaining genetic variation, this mainly focused on agricultural or forestry species, and used primarily *ex situ* approaches to genetic conservation (Hoban et al., *in prep*), such as captive breeding and seed banks. *Ex situ* approaches are usually implemented as a last resort, and only contain a 'snapshot' of a species' genetic diversity (Koskela et al., 2013). Thus, more attention to genetic conservation in wild species is needed, especially given proposed targets for CBD's post-2020 biodiversity framework to maintain genetic diversity within wild species (Hoban et al., 2020).

To meet these CBD targets, *in situ* conservation approaches must be designed to maintain genetic variation. For example, conserving populations deemed to be Evolutionary Significant Units (ESUs) (de Guia & Saitoh, 2007), e.g. Coho salmon *Oncorhynchus kisutch* (National Marines Fisheries Service, 2012), implementing genetic rescue and translocations to increase genetic diversity in populations (Fredrickson, Siminski, Woolf, & Hedrick, 2007; Johnson et al., 2010; Whiteley, Fitzpatrick, Funk, & Tallmon, 2015) or improving connectivity (i.e. dispersal and gene flow) between populations (Jangjoo, Matter, Roland, & Keyghobadi, 2016). These methods aim to conserve distinct populations *in situ* (ESU) or to increase genetic diversity in small wild populations. There are also

methods that specifically use genetic data to prioritise objectives for conservation management such as to prioritise connectivity or evolutionary potential (Nielsen et al., 2020). *In situ* conservation through Gene Conservation Units (GCUs) focuses on managing for genetic diversity in wild populations within defined areas (Maxted, Hawkes, Ford-Lloyd, & Williams, 2000). ‘Dynamic gene conservation’ is promoted in these areas by maintaining and managing populations in their natural habitats to allow adaptation to environmental changes through natural selection. By designating GCUs across the ecological range of a species, and managing these sites to allow reproduction and dynamic evolution, the GCUs conserve the adaptive genetic variation within species, and allow ongoing evolution and change. GCUs are novel in their emphasis on encouraging natural genetic adaptation, allowing populations in the wild to persist and adapt to future change, this dynamic process is particularly important in environments that are undergoing change. For current GCUs for trees, specific criteria are given including the population size and geographic size, to allow for dynamic gene conservation through natural regeneration (Koskela et al., 2013). However, this operationalization may not be applicable to other taxa and in different habitats.

In this policy perspective paper, we discuss current global application of *in situ* genetic conservation management techniques, considering whether the GCU approach could be effective for conserving evolutionary potential in a wide range of other taxa. We review current implementation of GCUs and use a structured questionnaire to canvass conservationists’ and land managers’ opinions concerning adopting a system of GCUs to protect biodiversity. We then test whether existing methods for voluntary accreditation of GCUs for trees (Koskela et al., 2013) are appropriate for application to other taxa, and recommend alterations to these methods, illustrating these recommendations for four case study species (*Erebia epiphron* (butterfly), *Bombus distinguendus* (bee), *Campanula rotundifolia* (plant) and *Hypocreopsis rhododendri* (fungus)). Our paper focuses on the UK, but the policy recommendations we develop are relevant for creating GCU networks across Europe and beyond.

2. Current implementation of GCUs and other *in situ* genetic conservation techniques

Firstly, we aimed to gain a better understanding of the taxa that are currently the focus of GCUs globally (we refer to any areas managed for genetic conservation as GCUs) and other *in situ*

conservation programmes including types of species and their socio-economic importance. Our literature review included published papers and ‘grey literature’ such as government/NGO reports. We extracted information on the focal species, the *in situ* genetic conservation method applied, and the reason for conservation action (economic or conservation importance) (see more information in Supporting Information Methods S1). We found genetic conservation implemented in 158 species, mostly trees and other plants (Supporting Information Figure S2). The most common programme was establishment of a GCU (72.8%), followed by assigning an ESU (without official ratification; 15.8%), and genetic rescue by translocation (8.9%), captive breeding (1.9%) or habitat connectivity (0.6%) (SI Figure S2). GCUs were selected to protect genetic resources of economically important plant species including about 100 tree species, and 10 species of crop wild relatives (SI Figure S2), such as citrus, wheat, maize and chilli. The European Forest Genetic Resources Programme (EUFORGEN) (www.euforgen.org) promotes conservation of genetic resources through a pan-European strategy for the establishment of GCUs (Koskela et al., 2013), resulting in over 3,200 GCUs harbouring more than 4,000 populations of about 100 tree species. A subsample of these form a core network which aims to capture current genetic diversity across Europe for a number of forest tree species by representing populations from different local climate and environmental conditions. Therefore, GCUs have been successfully used to protect genetic diversity in mainly economically important plant species in the wild. The proposed future CBD targets focus on protecting genetic diversity within all wild species (Hoban et al., 2020), making it vital to explore the potential to extend the GCU approach to other plant and animal taxa.

3. Exploring the scope for implementing GCUs more widely as a technique to conserve genetic diversity

We used a structured questionnaire to canvass conservationists’ and land managers’ opinions concerning adopting a system of GCUs to protect biodiversity. We want this GCU method to be something that is co-developed with stakeholders so that it is something that practitioners and land managers are willing to sign up for, and therefore any concerns and benefits were important for us to understand. Our experience suggests that a co-development approach is likely to appeal to land

managers as it gives them greater ownership of the process (O'Brien et al. 2021). We received responses from 60 UK participants including researchers (26%), non-governmental organisations (33%), private land managers (7%), government/non-departmental public bodies (24%) and others (4%) (SI Figure S3). Responses provided information on current genetic practises and support for developing GCUs for species conservation, including opinions on perceived risks, benefits and feasibility of GCUs (see S1 Methods). This information provided insight into the scope for GCU implementation, and whether existing methods could be applied to other species. Genetic conservation is valued in the UK (SI Figure S4, S5, S6) and *in situ* genetic conservation management has focused on plant species (Figure 1B, 1C), confirming the findings from our literature review. Most organisations surveyed do not have a genetic conservation policy (SI Figure S5C), although many participants considered that genetic information should be more integrated into conservation in the future (Figure 1A). The main perceived barriers to implementing genetic conservation management are lack of specific knowledge and financial constraints (Figure 1D). These hamper progress, despite support for integrating genetic information into conservation management in the UK. Therefore, there is merit in exploring the feasibility of extending GCU policy to include all species so that, when accompanied by simple guidelines, GCUs may serve as a genetic conservation technique which could be implemented by land managers.

Conservationists and landowners listed several perceived benefits of GCUs (Figure 2A, 1B). The most frequently mentioned was maintaining genetic diversity and adaptability of populations, allowing them to persist and continue to adapt in response to environmental changes and other challenges. The most frequently cited benefits for landowners related to financial gains (e.g. benefits to economically exploited species, attracting public funding), prestige and pride that land managers experienced when conserving their land for species resilience, and wider conservation benefits (e.g. increasing connectivity, GCUs acting as gene banks). The role of GCUs in raising awareness of the importance of species conservation was often mentioned as a general benefits or a benefit to landowners, with a recognition that more awareness and engagement on the importance of genetic diversity and adaptability could promote genetic conservation activities in the future. Respondents also suggested

several potential risks of designating populations as GCUs (Figure 2C), including neglecting non-target species, overlooking populations outside of the GCU and negative genetic consequences, including inbreeding. There were mainly positive responses regarding the potential to recognise GCUs for more mobile target species such as large mammals, insects and birds (Figure 2D). Respondents considered that to make them applicable to more mobile species, GCU boundaries should be flexible, accounting for dispersal distances, with adaptable criteria to suit species' characteristics such as population size and geographical scale. Another concern was that future climate change may displace populations uphill or to more northern latitudes (i.e. poleward), and that GCUs may need to move with them.

There were mixed responses regarding the potential for GCU management to conflict with current management actions (Figure 2E). While some stated that the GCU would enhance the existing management plans, others stated that there could be conflicts if the area was not already managed for the conservation of the focal species. Other conflicts raised included concerns that current management plans might fail to recognise genetic diversity and evolutionary processes, for example if 'pure bred' conservation measures are in force e.g. deliberately removing hybrids. Similarly, some responses expressed concern for 'keeping things apart' rather than allowing mixing and gene flow in the area. However, although one objective of GCUs for trees is to protect adaptive traits, other objectives are to encourage dynamic gene conservation, through natural processes which may involve mixing and connecting-up habitats. Similarly, a new objective for GCUs for other taxa may be to increase genetic diversity, thereby introducing new genes through captive breeding or translocations from elsewhere. Most respondents whose answers were grouped into 'yes' or 'possibly' gave some advice to reduce these potential conflicts, including having flexible criteria, and working alongside land managers to fully integrate the GCU management plan into existing plans. Some respondents also expressed concern for yet another system of registering sites of high conservation interest, and suggested that instead of a standalone scheme, GCUs could be integrated with current practises.

Therefore, responses indicate general support from conservationists and land managers for the GCU approach for other taxa, as well as raising some concerns. To address these concerns, we propose a

flexible approach, including voluntary certification (not statutory designation) with simple standardised selection criteria that can be adapted for each target species or group of target species. This would allow GCU boundaries to move, for example if populations are displaced uphill or northwards under future climate change. To explore how GCU criteria may need to be tailored to suit particular species, we consider four exemplar case study species.

4. Developing GCU guidance to protect a wide range of species: four case study species

EUFORGEN has developed minimum criteria for registering populations as GCUs on the publicly available EUFGIS database (Koskela et al. 2013). GCUs for forest tree species must have a management plan, at least one target species, with a breeding population of at least 50 (marginal or scattered tree populations) or 500 (stand-forming conifer or broadleaf species) individuals. To explore the feasibility of developing GCUs for species other than forest trees, we selected four species to act as test cases and developed criteria specific to each. These case study species differ in their level of genetic risk and population dynamics, but are all of conservation importance in the UK (Table 1). These differences between species highlighted the need to retain certain criteria and to revise or introduce others.

4.1 Deciding on the effective population size for GCU

The minimum size of a genetically viable population (or breeding population) is defined as $N_e = 500$ where the goal is to maintain long-term evolutionary potential in a population (Franklin, 1980), and this is incorporated into the GCU forest guidelines to protect genetic diversity and ensure continued evolutionary processes (Koskela et al. 2013). An N_e of 500 is also suggested for any initiative for the conservation of genetic diversity in wild populations (Hoban et al., 2020). N_e can be inferred from N_c which represents a population census, and a N_e of 500 roughly equates to an N_c of 5,000, however there is variation in this ratio among taxa (Hoban et al., 2020). A universal ‘rule of thumb’ N_e or N_c for inclusion in a GCU would be difficult to put into practice as these numbers will vary considerably among taxa. For example, breeding populations may represent individuals, however, in eusocial species such as bumblebees, each nest represents one breeding unit. In practice identifying 5,000

individuals in an area would be unrealistic for many species. Thus, rather than providing a set N_e or N_c value, we suggest that the population size threshold for inclusion in a GCU needs to be taxon specific and calculated using information on the species biology.

4.2 Recommended GCU criteria appropriate for each case study species

Bombus distinguendus

The number of great yellow bumblebee *Bombus distinguendus* breeding colonies among different sites across its distribution range from 12 – 63, with a mean of 25 (Charman, Sears, Green, & Bourke, 2010). The population density of the great yellow bumblebee is 19.3 nests per km² of suitable habitat (Charman et al., 2010). Gene flow occurs within Scottish island groups (SI Figure S7A), but little occurs between them (Charman et al., 2010), therefore it would be appropriate to designate a GCU for each island group (Orkney, Outer Hebrides, Inner Hebrides) and the mainland population. Therefore, GCUs could be designated to incorporate the total area of occupied suitable habitat (> 2km²) in the islands and mainland group, with conservation management to increase gene flow within each group.

Erebia epiphron

The mountain ringlet butterfly, *Erebia epiphron*, (UK distribution: SI Figure S7B) occurs in discrete colonies where they are locally abundant, but with little dispersal between populations (Czech populations; Kuras, Benes, Fric, & Konvicka, 2003). Designated GCUs should include the entire metapopulation (e.g. Eastern Lake District, England or Ben Lawers, Scotland) and should contain suitable upland habitat, with appropriate grazing regimes (Ewing et al., 2020).

Hypocreopsis rhododendri

Hazelgroves, *Hypocreopsis rhododendri* (UK distribution: SI Figure S7C) is a parasitic ascomycete fungus which requires abundant host populations, the wood decaying ‘glue fungus’ *Pseudochaete corrugata* (Grundy, Woodward, Genney, & Taylor, 2012). The number of breeding individuals is unknown but the presence of the host fungus may be used as an effective proxy to indicate the population number for the parasite. Further understanding of this species’ biology, along with

demographic and genetic data for the host fungus, are required before GCU design can be considered.

This case study species highlights the importance of information on species' biology to design GCUs.

Campanula rotundifolia

Harebells *Campanula rotundifolia* are widespread but declining (UK distribution: SI Figure S7D) and form four cytotypes (differences in the number of sets of chromosomes), three of which occur in the UK: tetaploid, pentaploid and hexaploid (Wilson et al., 2020). GCUs could be created in different areas of the range to incorporate different cytotypes. *C. rotundifolia* is locally common in tall-herb grassland habitats (Stevens et al., 2012), so we suggest a GCU area which incorporates the entire occupied grassland in a particular site.

5. Management recommendations

Considerable time and thought have been invested in developing the concept of GCUs for *in situ* conservation of forest tree species and here we explore the support for, and the feasibility of, using this approach across a wider range of species as a means of achieving the CBD Aichi target of maintaining genetic variation. Our study suggests that GCUs could conserve genetic diversity in a wide range of target species and we present guidelines for the minimum qualification criteria that must be met for GCU certification (Box 1). As such GCUs could be classed as ‘other effective area-based conservation measures’ (OECMs): areas that are achieving effective *in situ* conservation of biodiversity outside of protected areas (CBD, 2018).

Some GCU criteria used for forest trees remain appropriate for GCUs for other taxa (Box 1, Criterion A, B, F & G) (Koskela et al. 2013). However, other criteria must be tailored to particular species (Box 1, Criterion C, D & E). Firstly, the breeding population size (N_e) of the target species must be calculated species-specifically, and it is not appropriate to apply a single ‘rule of thumb’ N_e for multiple taxa (Box 1, Criterion C). Secondly, the land area of a GCU should be inferred by the space required to support a minimum breeding population, and will differ depending on the target species’ mobility and dispersal characteristics (Box 1, Criterion E). The distribution of the breeding population for inclusion in the GCUs will depend on the species distribution type (distinct or local, metapopulation or continuously distributed) (Box 1, Criterion D), which can be identified on the basis of genetic, demographic or ecoregion data. GCUs for species with continuous populations can be identified using ecoregions (different climatic zones). Genetic data could be used to identify genetic diversity ‘hotspots’, or to select populations based on the objective to prioritise connectivity or evolutionary potential (see Nielsen et al., 2020). As with GCUs for forest trees, those for other taxa will not be statutory designations and therefore there will be flexibility as long as the minimum viable population is maintained.

The operationalization of a GCU for trees is to encourage dynamic gene conservation by recognising appropriate breeding populations in a geographic area to manage these populations to promote regular cycles of natural regeneration to occur. For other taxa, the operationalization of GCUs must similarly

promote the occurrence of natural regeneration or reproduction. This will be achieved through conservation management actions listed in the management plan that promote persistence of the focal species, and mitigate genetic threats. Depending on the conservation objective of the GCU (Box 1, Criterion B), this may for example involve connecting up habitats to increase gene flow, or translocating individuals (genetic rescue) into the GCU to increase genetic diversity. Genetic and population monitoring of focal populations would also be appropriate to ensure sufficient population sizes for reproduction and healthy genetic diversity.

Although we have described some enthusiasm for the efficacy and feasibility of the GCU system for multiple taxa, alternatives to this method were suggested by some respondents to our questionnaire. Some individuals stated that rather than a stand-alone scheme, the GCU objectives could instead be integrated into existing land protection methods. However, a caveat to this suggestion is that GCUs would be a voluntary certification, allowing more land owners and conservation bodies to register their land if it meets the GCU general criteria.

We have highlighted how existing methods for GCU designation could be altered for other taxa, however deciding which taxa should be the focus of a GCU is something which needs to be further explored, and is beyond the scope of this paper. Whether GCUs could be used for multiple taxa or may be more species-specific, along with the types of species to include, are all issues which need to be further discussed with stakeholders. Species prioritisation tools could be used, such as selecting species based on their socio-economic and/or cultural value (Hollingsworth et al., 2020) or combining criteria based on species value, management costs, and threat status (Joseph et al., 2009).

6. Conclusions and next steps

There is a need to develop a system for *in situ* genetic conservation. By building on the GCU approach successfully applied to trees in Europe, it will be possible to develop a system that is low cost to participants and that can coexist with current management practices, and one that aligns with proposed expansion of ‘other effective area-based conservation measures’ (CBD 2018). For land managers to register sites as GCUs, funds are required to establish and maintain an international

database, such as EUFGIS for tree species, where common criteria are applied for the listing of GCUs of a given species and the same descriptors are used to characterise the selected populations. These data could then be used to select populations to establish a core network of GCUs for each species that would capture the diversity across its distribution range. Additionally, further investigation into the application of GCUs for other taxa requires additional discussion about how to prioritise species for GCUs, for which we have set up a Gene Conservation Unit working group, to facilitate discussion and make key decisions on taking this approach forward to implement the first non-tree GCU.

Acknowledgments

We acknowledge the funding contributions for this project, M.M. was supported under a NERC NPIF iCASE studentship NE/P009417/1. Ethical approval for the research was granted by the University of York, Department of Biology Ethics Committee (Reference: MM202004). We thank the following: the 60 land managers and conservationists who completed the questionnaire, and whose responses helped shape this paper; Annie McKee and Caroline Ward for their useful comments on the draft questionnaire; Julia Wilson for advice regarding GCUs for Harebells; David Genney, NatureScot, Lorne Gill and the Royal Botanic Garden Edinburgh for the use of species photos.

Author contributions

M.M., D.O. and J.H. conceived the ideas; M.M. collected the data; M.M. analysed the data; M.M. drafted the manuscript; all authors contributed to the final manuscript.

Data Availability Statement

Ethical approval for this project states that questionnaire responses must remain anonymous and therefore this data cannot be shared. Literature review data is available from the Dryad Digital Repository: <https://doi.org/10.5061/dryad.3j9kd51hm> (Minter et al., 2021).

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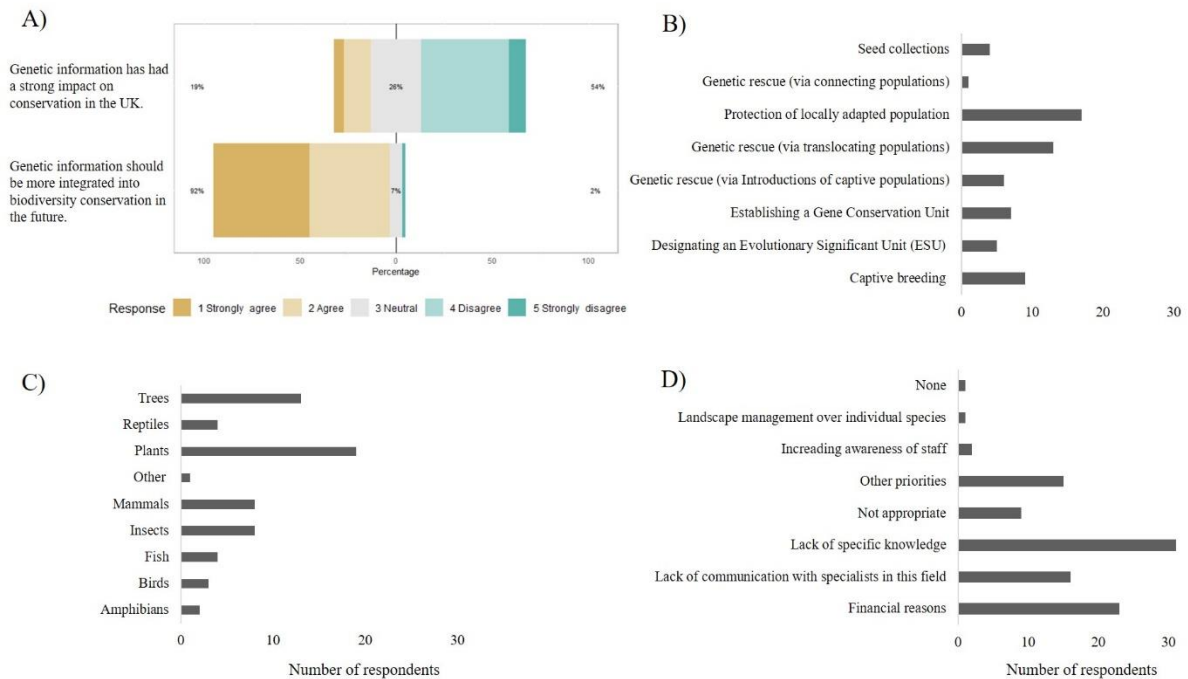


Figure 1: Current *in situ* genetic conservation implemented by conservationists and land managers A) Opinions of current and future implementation of genetic conservation, responses to statements were collected in a Likert scale, B) Types and frequency of genetic conservation management currently implemented, C) Type and frequency of taxa included in genetic conservation management and D) Perceived barriers to implementing genetic conservation management.

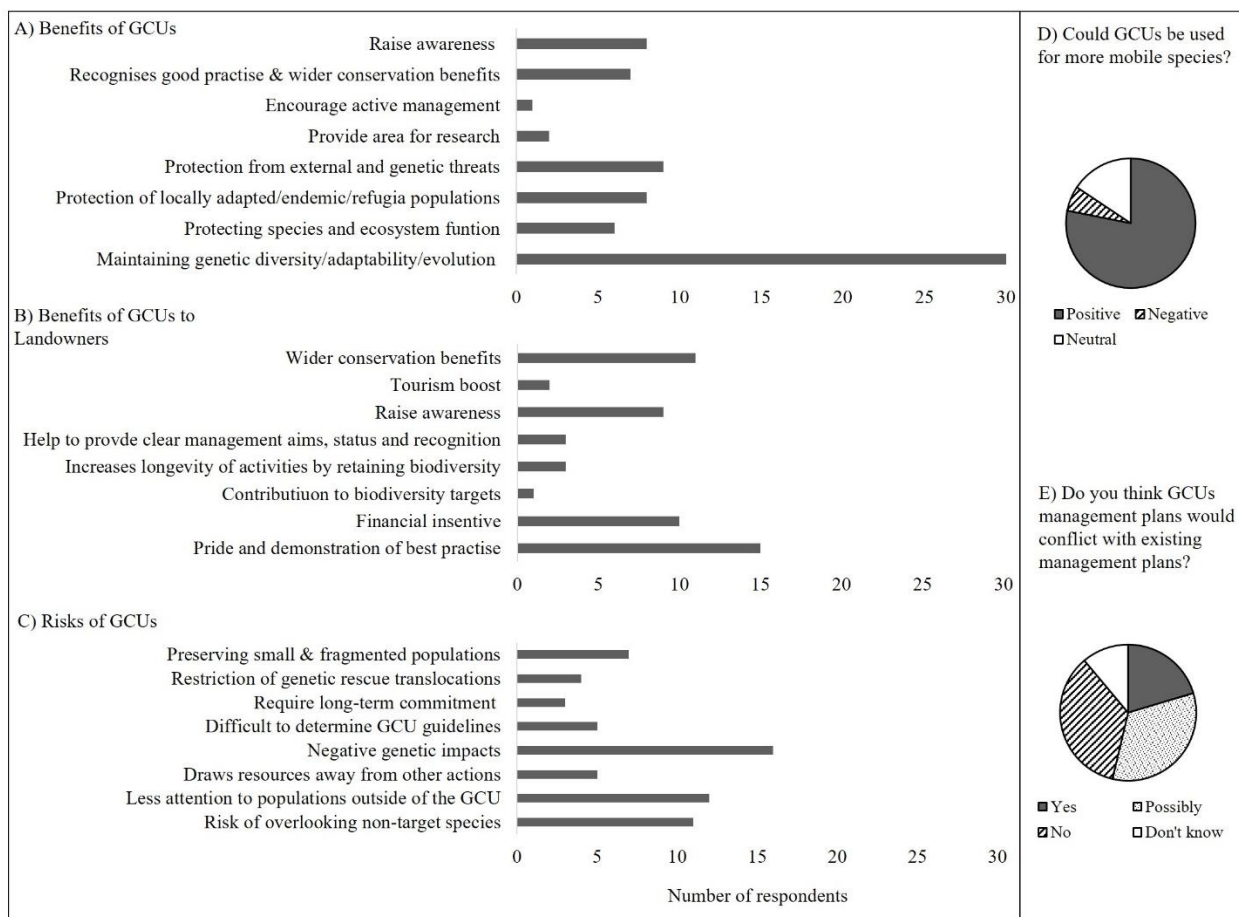


Figure 2: Questionnaire responses of 60 conservationists and land managers to test the feasibility, risks and benefits of extending the GCU concept to other species, (open ended answers grouped into broad categories) A) Perceived benefits of GCUs, B) Perceived benefits of GCUs specifically to land managers, C) Perceived risks of GCUs, D) Perceived feasibility of extending GCUs to include more mobile species E) Perceived conflicts of GCU management plans with existing management plans





Species & genetic risk	UK population threats	Contribution of UK population to species diversity	Genetic risks	GCU selection criteria
Mountain ringlet <i>Erebia epiphron</i> : Moderate 	<ul style="list-style-type: none"> Climate change 	<ul style="list-style-type: none"> High unique genetic diversity in England Low elevation range edge 	<ul style="list-style-type: none"> Risk of loss of English genetic diversity 	<ul style="list-style-type: none"> Area to include metapopulation GCU to capture unique genetic diversity in England/allowing natural adaptation to climate change
Hazel gloves <i>Hypocrepis Rhododendri</i> : Negligible 	<ul style="list-style-type: none"> Heavy grazing Habitat change Invasive spp 	<ul style="list-style-type: none"> Bottleneck in Scottish populations Source populations in N America higher genetic diversity 	<ul style="list-style-type: none"> No evidence of adaptive variation Little risk as Scottish genetic diversity is a subset found elsewhere 	<ul style="list-style-type: none"> Area = could not be determined More data required
Great yellow bumblebee <i>Bombus distinguendus</i> : Serious 	<ul style="list-style-type: none"> Habitat loss Climate change 	<ul style="list-style-type: none"> Scotland holds last remaining genetic diversity from UK 	<ul style="list-style-type: none"> Genetic diversity already lost due to declines Low genetic diversity 	<ul style="list-style-type: none"> Area to include total area of suitable habitat GCU in within each island group and mainland
Harebell or Scottish bluebell <i>Campanula rotundifolia</i> : Moderate 	<ul style="list-style-type: none"> Habitat loss (through agricultural intensification & woodland regeneration) 	<ul style="list-style-type: none"> UK contains three cytotypes: tetraploid, pentaploid and hexaploid 	<ul style="list-style-type: none"> Potential hybridisation with non-native genotypes Declines in Scotland would impact hexaploid cytotype 	<ul style="list-style-type: none"> Area to include the entire grassland habitat GCU across the different cytotypes

Table 1: Case study species of UK conservation importance used to create selection criteria for GCU. The four case study species vary in genetic risk, population dynamics and taxa to understand whether criteria can be designed for different species of varying genetic importance. GCU criteria is suggested for all species, with Hazelgloves requiring more demographic data to determine GCU criteria. References: Mountain ringlet: Franco et al., (2006), Minter et al., (2020) Hazelgloves: Grundy et al., (2012); Great yellow bumblebee: Charman et al., (2010), Harebell: Stevens, Wilson, & McAllister (2012), Wilson et al., (2020). Genetic risk derived from Hollingsworth et al., (2020).

Box 1: Gene Conservation Unit criteria for terrestrial species

Criterion A: At least 1 target species must be included in the GCU

Multiple target species can be included if they meet species criteria

Criterion B: Conservation objective

Bi) To maintain genetic diversity

Bii) To conserve adaptive or other traits in distinct population

Biii) To increase genetic diversity (with additional methods e.g. captive breeding or translocation)

Criterion C: Population size

Breeding population should be tailored to species specific requirements and depending on distribution (Criterion D) and biological characteristics

Criterion D: Distribution

Di) Distinct or local

Dii) Metapopulation

Diii) Continuous distribution

Criterion E: Land area

Land area must contain the appropriate breeding populations of target species and appropriate habitat cover

Criterion F: Management objectives

Fi) Maintaining genetic diversity must be key management goal

Fii) Ensure continued existence of target species

Fiii) Create favourable conditions and actions to mitigate genetic threats for target species through habitat management

Criterion G: Monitoring

Gi) Field surveys are undertaken to monitor population size of target species

Gii) Field visits to ensure favourable conditions for target species are maintained

Criterion H: Database

GCU must be listed on a publicly accessible database which has clear definitions of the data to ensure consistency.

Supporting Information

Methods S1

Literature review

We conducted a systematic literature review (published papers and ‘grey’ literature) to search for evidence of genetic conservation in the literature. Only studies where the main or one of the main purposes of the conservation was to protect or increase genetic diversity were included. Searches in the literature include ‘genetic rescue’, ‘gene reserves’, ‘genetic conservation unit’, ‘evolutionary significant unit’. Further literature was obtained through references within this literature. For each study, the name of the species along with the type of genetic conservation management was extracted. The species were then categorised into species group (trees, mammals, plants (not trees), birds, reptiles, amphibians and fish) and socio-economic value (conservation, timber, craft, medicinal, game, fisheries, agriculture and ornamental). Data from the literature review is available from the Dryad Digital Repository: <https://doi.org/10.5061/dryad.3j9kd51hm> (Minter et al., 2021).

Questionnaire

To understand how different stakeholders including conservationists and other land managers perceive the importance of genetic diversity, and to gather information about current approaches to genetic conservation in the UK a questionnaire was designed. The questionnaire was made up of four sections: 1) information about the participant (organisation sector), 2) their perceptions of genetic conservation (including perceived importance, perceived impact of genetics on UK conservation), 3) their understanding of current genetic conservation in the UK (if genetic data were used to inform conservation management, what genetic conservation has been implemented, which species this had been focussed on) and 4) their understanding of the concept of Gene Conservation Areas (including risks and benefits) (see Questionnaire SM 8). Sections 1-3 are mostly made up of questions with standardized answers, and section 4 contains questions with open-ended questions to get detailed input from participants. A variety of stakeholders was targeted for this study, including NGOs, land managers (i.e. including farming and estate management), government/non-departmental public bodies and research institutes/universities.

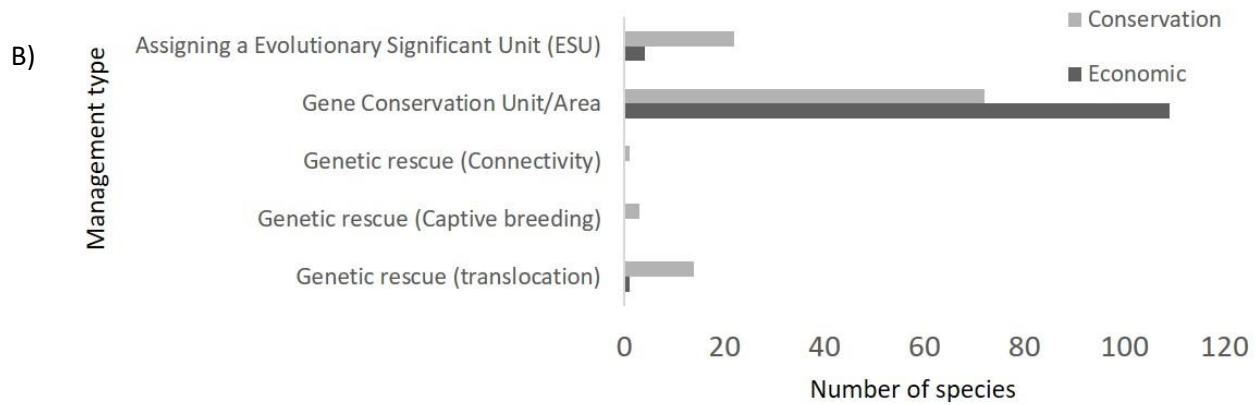
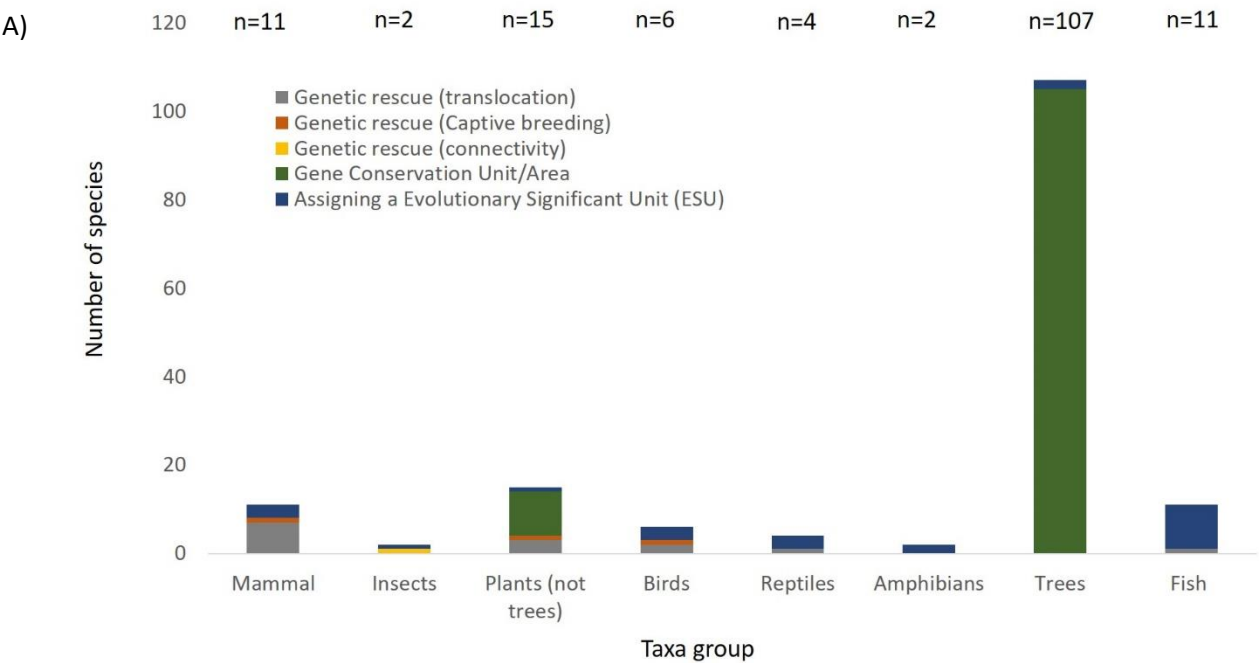


Figure S2: A) Number of species which *in situ* genetic conservation management strategies have been implemented on, grouped by taxon and management type, B) and split by management type and reason for conservation action, either species of conservation value or economic value, such as agriculture, forestry, game etc.

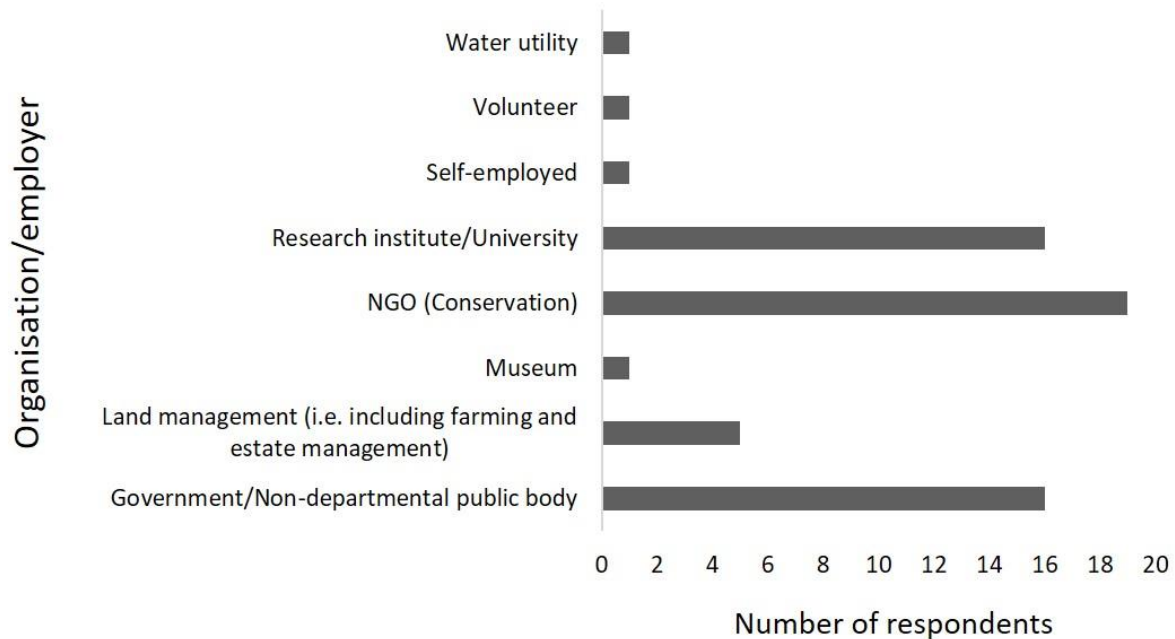


Figure S3: Questionnaire respondents and their employer $n=60$



Figure S4: Word cloud of the open ended answers to Question 6 of the Questionnaire: “What do you think are the benefits of conserving genetic diversity?” Size of word represents frequency of word mention. Word cloud created at <https://wordart.com/>



Figure S5: Questionnaire response to questions about the use of genetic information and research to guide management practises in the UK

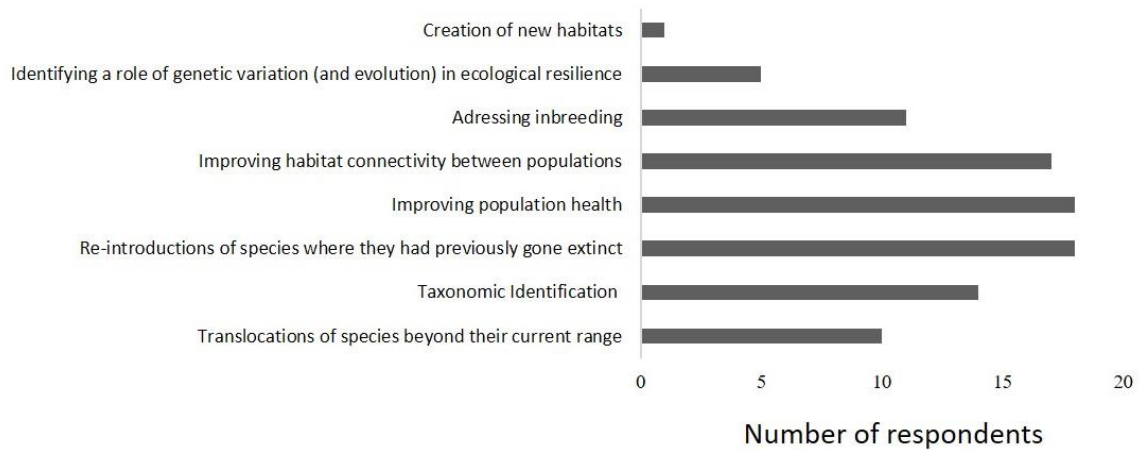


Figure S6: The reasons for which genetic information has been incorporated into species conservation in the UK

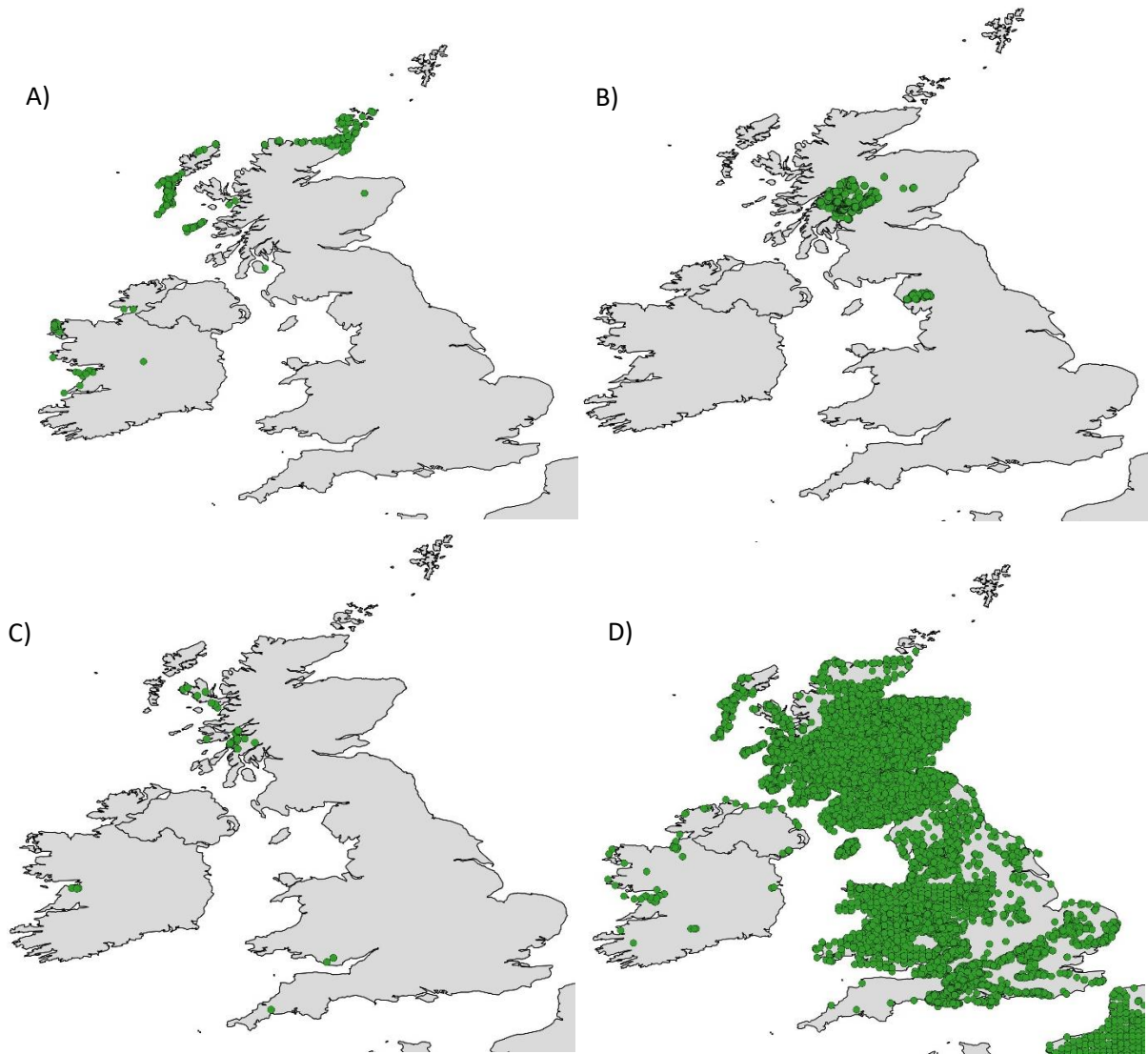


Figure S7: Case species UK distribution (green circles) A) *Bombus distinguendus* Great yellow bumblebee, data 1995-2020 from GBIF (<https://www.gbif.org/>), B) *Erebia epiphron* Mountain ringlet, data 1970-2014 UK Butterfly Monitoring Scheme data (<https://www.ukbms.org/>), C) *Hypocrepopsis rhododendri* Hazelgloves fungus 1970-2020 from GBIF, D) *Campanula rotundifolia* Harebell 1970-2020 from GBIF

Questionnaire S8: Questionnaire which was sent to conservationists and land managers in the UK including information for participants, consent form and the Questionnaire

Genetic conservation in the UK: Gene Conservation Areas (GCA), broadening the concept beyond trees

1. Information for participants

We would like to invite you to take part in our research study. Before you decide we would like you to understand why the research is being done and what it would involve for you. We understand that this is a difficult time under the current COVID-19 pandemic, and so we understand if this is not an appropriate time to be involved in this research study which is part of a PhD project at the University of York and Scottish Natural Heritage.

In our study we aim to understand perceptions of genetic conservation in the UK, the role of genetics in conservation management, and to explore whether, and how, Gene Conservation Areas (GCA) could be used as a genetic conservation management tool for other species beyond trees.

Genetic information from DNA sequencing of wild populations has increased over the last 30 years, along with understanding the role of genetics in supporting the resilience of species and habitats. We want to understand how people perceive the role of genetics in conservation management. We also want to understand whether you are using genetic data in conservation management, or implementing specific management to protect genetic diversity or to increase genetic health.

The first Gene Conservation Area (also known as Gene Conservation Unit for trees) in the UK was designated at Beinn Eighe in Scotland in 2019, to protect the genetic diversity of population of Scots pine tree. For information on this genetic reserve please see the following BBC article:

Genetic reserve in Wester Ross to protect Scotland's national tree

By Ken Macdonald
BBC Scotland Science Correspondent

20 March 2019

f     Share



<https://www.bbc.co.uk/news/uk-scotland-47633399>

The concept of Gene Conservation Units (GCU) for trees was established over 20 years ago, and these reserves can be found all over Europe. GCUs were established to allow dynamic gene conservation to take place, which means the protection of natural processes in the area, and allowing genetic changes to develop naturally in response to changes in the natural environment e.g. climate change. Forest Research has put together guidelines for establishing and managing Gene Conservation Units for trees which can be found here:

<https://www.forestresearch.gov.uk/research/establishing-and-managing-gene-conservation-units/>.

In this survey, we want to gather information on Gene Conservation Areas (GCA), which would extend the GCU approach to other species. We want to explore whether this same approach could be used on other species beyond trees, and therefore we want to gather information on the perceived risks and opportunities of this. If this could be applied to other species, then a registration scheme would be produced and used to inform future management guidelines. We will use your responses in this survey to develop these ideas.

2. What information is being collected?

We are gathering information from different stakeholders including conservationists and other land managers. The questionnaire is divided into 4 main sections, containing 22 questions and should take about 20 minutes to complete. There are no wrong or right answers, we are primarily interested in your personal opinions (except section 3 on current genetic conservation):

Part 1: Information about you

Part 2: Your perceptions of genetic conservation

Part 3: Your understanding of current genetic conservation in the UK

Part 4: Your understanding of the concept of Gene Conservation Areas

3. Why do we need your personal information, and how will it be used?

Neither you nor your organisation will be identified in any of output (e.g. report) arising from the research. Your name, contact email and company name will be kept separate from the rest of the data, and would only be used 1) (to identify your response) in the event that you wished to withdraw your response after submission and 2) if there is any follow-up study where we may invite you to participate. We request information on your employer type (e.g. NGO, research institution, land agency, estate company etc) so that we can compare responses between sectors. Both the pseudonymised research data, and your personal information, will be stored securely to ensure confidentiality. All personal data will be destroyed upon completion of the PhD project, in 2022. Participants can withdraw from the survey at any time and request their data to be withdrawn. We request written informed consent (electronic form) at the start of the questionnaire where you will also find our privacy statement. The survey conforms to all ethical approvals required by University of York Department of Biology Ethics Committee.

If you have any questions about the project or data collection, you can email Melissa Minter mm1874@york.ac.uk.

Consent form

Please also see the privacy notice statement

I confirm that I have read and understand the information sheet explaining the research project and I have had the opportunity to ask questions (by email if required) about the project.

681 Yes

682 No

683 I give permission for the PhD student and the PhD student's supervisor to have access to my
684 pseudonymised responses and personal data kept separately. I understand that my name will not be
685 linked with the research materials, and I will not be identified or identifiable in the report or reports
686 that result from the research. I understand that my responses will be kept strictly confidential.

687 Yes

688 No

689 I understand that my participation is voluntary and that I am free to withdraw at any time (until the
690 completion of the project) without giving any reason and without there being any negative
691 consequences. In addition, should I not wish to answer any particular question or questions, I am
692 free to decline. I can indicate a wish to withdraw by informing Melissa Minter
693 (mm1874@york.ac.uk). At the start of 2022 all personal data will be destroyed, and the data will
694 become fully anonymised. After this point it will no longer be possible to withdraw your response.

695 Yes

696 No

697

698 I agree for my personal information to be stored securely, separate from the pseudonymised data. I
699 am happy to be contacted by the email I provided if any follow-up study was conducted before all
700 personal data is destroyed in 2022.

701 Yes

702 No

703

704 I agree for the data collected from me to be stored and used in relevant future research in an
705 pseudonymised form

706 Yes

707 No

708

709 I understand that relevant sections of the data collected during the study may be looked at in
710 pseudonymised aggregated format by individuals from Scottish Natural Heritage or University of
711 York. The data will be aggregated to ensure individuals or organisations could not be identified from
712 questionnaire responses. I give permission for these individuals to have access to my pseudonymised
713 aggregated data.

714 Yes

715 No

716

717 Please enter your initials and date to complete consent

718

719 Questionnaire

720 Part 1: Information about you

721 1. *What is your name?*

722

723 2. *What is your contact email?*

724

725 3. *What is the name of your organisation/employer?*

726

727

728 4. *Please select the most relevant to your organisation/employer*

729 NGO (Conservation)

730 NGO (Other)

731 Land management (i.e. including farming and estate management)

732 Government/Non-departmental public body

733 Research institute/University

734 Self-employed

735 Other

736 *If 'Other' please specify*

737

738 Part 2: Your perception of genetic conservation

739 5. *Do you think genetic diversity is important to species survival?*

740 0 Don't know

741 1 Very important

742 2 Important

743 3 Neutral

744 4 Less important

745 5 Not important

746

747 6. *What do you think are the benefits of conserving genetic diversity?*

748

749 7. *Please state how much you agree or disagree with the following statement: Genetic information has had a strong impact on conservation in the UK.*

750 0 Don't know

751 1 Strongly agree

752 2 Agree

753 3 Neutral

754 4 Disagree

755 5 Strongly disagree

756

757

8. *Please state how much you agree or disagree with the following statement: Genetic information should be more integrated into biodiversity conservation in the future.*

0 Don't know

1 Strongly agree

2 Agree

3 Neutral

4 Disagree

5 Strongly disagree

Part 3: Implementation of genetic conservation

This section is to understand how genetics is being used currently in the UK within conservation. This section may be more applicable to those who work in land and conservation management. **If this section is not applicable to you, please skip to part 4.**

9. *Have you or your organisation incorporated genetic information or techniques into species conservation?*

Yes

No

Don't know

10. *If the answer to question 9 was 'Yes,' what did this conservation action seek to address? Please tick all that apply*

Re-introductions of species where they had previously gone extinct

Translocations of species beyond their current range

Improving population health

Improving habitat connectivity between populations

Addressing inbreeding

Taxonomic identification

Other

If 'Other' please specify

Any additional comments:

11. *Have you or your organisation used genetic information to guide your management recommendations?*

Yes

No

Don't know

Any additional comments:

12. *Have you or your organisation genetic scientific research to guide your management recommendations?*

Yes

No

Don't know

Any additional comments:

13. *Have you or your organisation implemented any conservation management to specifically conserve genetic diversity?*

Yes

No

Don't know

14. *If the answer to question 13 was 'Yes' please specify what kind of conservation management this was:*

Genetic rescue (via Introductions of captive populations into the wild to increase genetic diversity)

Genetic rescue (via translocating populations to increase genetic diversity)

Captive breeding

Establishing a Gene Conservation Unit

Protection of locally adapted population

Designating an Evolutionary Significant Unit (ESU) (population of organisms that is considered distinct to the rest of the species)

Other

If 'Other' please specify

Any additional comments:

15. *If the answer to questions 13 was 'Yes' what species group was this conservation action focused on? Please tick all that apply*

Plants (not trees)

Trees

Mammals

Invertebrates

Birds

Reptiles

Amphibians

Fish

Other

16. Does your organisation have a genetic policy in respect to conservation?

Yes

No

Don't know

If 'Yes' can you please specify

17. *What are the barriers to implementing genetic conservation management for you or your organisation?*

Financial reasons

Not appropriate

Other priorities

Lack of specific knowledge

Lack of communication with specialists in this field

Other

If 'Other' please specify

Any additional comments:

Part 4: Gene Conservation Areas: a concept beyond trees?

In this section, the questions are open-ended, as we wish to gather your opinions on the concept of GCAs for genetic conservation of species. If GCA certification is implemented for species other than trees, we want to ensure this would benefit land owners and would not conflict with existing conservation management plans.

18. *Please can you describe the potential benefits of GCAs for gene conservation*

19. *Please can you describe the potential risks of GCAs for gene conservation*

20. *Please can you describe the benefits of GCA certification for landowners*

21. *GCAs have been established to protect trees and 'crop wild relatives' (a wild plant closely related to crop species). Do you think this GCA concept could work in more mobile species such as mammals, insects, birds etc?*

22. *Do you think implementing a GCA management plan could conflict with existing conservation management plans?*

898
899
900
901
902
903

23. Please add any further comments.